Amendments to the Specification

Please replace paragraph [0192] of U.S. Publication No. 2008/0153104 of the present specification or page 39, line 19 of the present specification as originally filed with the following amended paragraph:

[0192] The identity of a nucleotide sequence can be determined by using the algorithm BLAST by Karlin and Altschul (Proc. Natl. Acad. Sci. USA, 90: 5873-5877, 1993). The programs called BLASTN and BLASTX have been developed based on the above algorithm (Altschul et al., J. Mol. Biol., 215: 403-410 1990). In the case of analyzing a nucleotide sequence by BLASTN based on BLAST, the parameters can be set, for example, score = 100 and wordlength = 12. BLAST and Gapped BLAST programs may be used with its default parameter. The specific techniques of these analysis methods are known in the art (~~http://www.ncbi.nlm.nih.gov~~).

Please replace paragraph [0228] of U.S. Publication No. 2008/0153104 of the present specification or page 50, line 14 of the present specification as originally filed with the following amended paragraph:

[0228] In another aspect, the present invention provides a method of diagnosing cancer by detecting C20orf102 protein. The method of the present invention is characterized by detecting C20orf102 protein. C20orf102 is a secretory protein with a secretory signal at the N-terminus, and its amino acid sequence and the gene sequence encoding this sequence are described in GenBank Accession No. NM_080607 (SEQ ID NOs: 2 and 66). In the present invention, C20orf102 protein encompasses both full-length protein and a fragment thereof. The fragment is a polypeptide containing a given domain of C20orf102 protein and it may not have a function of natural C20orf102 protein. The secretory signal of C20orf102 protein corresponds to 1 to 24 amino acids in the amino acid sequence represented by SEQ ID NO: 66 (~~Psort Prediction: http://psort.nibb.ac.jp/~~).